Automated Change Detection in Serial Imaging Studies of the Brain
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Background

Much of the practice of radiology is focused on detecting and characterizing changes in images, usually to assess the effects of therapy. This presentation will focus on computer algorithms we have developed to detect and characterize changes, as applied to brain gliomas. It is also known that human measurements of disease suffer poor reproducibility, reducing sensitivity to small changes. Because available treatments result in patient morbidity and are expensive, getting early information about treatment effects can relieve suffering and reduce healthcare costs. To address this shortcoming, we have developed a new methodology for detecting and characterizing changes between 2 imaging examinations, which we call “Change Analysis.”

Methods

The change analysis algorithm consists of several steps that ultimately produce quantitative change maps (see Fig 1). The images used for this analysis are standard clinical pulse sequences: T1, T2, FLAIR, and T1-post contrast. All images were acquired in the oblique-axial plane with 3 or 4mm thick slices and 0 gap on standard clinical scanners. The first step consists of spatial alignment of all pulse sequences. We use the normalized mutual information algorithm as implemented in the Insight Toolkit (www.itk.org) and use the post-contrast T1 sequence of the newer examination as the template. To reduce field heterogeneity effects, we apply the N3[1] correction to all images.

At this point, a human defines samples of normal appearing white matter (NAWM). Typically, about 100 points are used. We have developed an algorithm for automatically defining the clusters for samples of other tissues of interest, including gray matter (GM), cerebrospinal fluid (CSF), non-enhancing T2 abnormality (NETTA), enhancing tissue (ENH), and necrotic tissue (NEC). These sample points are computed by computing their typical intensity relative to the NAWM sample provided on each of the pulse sequences, and then ‘looking’ for populations of voxels in anatomically reasonable locations.

Once tissue intensity clusters have been determined, feature images are produced for each tissue type, for each time point. This is done by linearly recombining the original pulse sequences by perpendicularly projecting in feature space the intensities of each voxel, onto lines connecting the centroids of the relevant tissue pairs.

In the next step, the algorithm determines the most likely transition for each voxel. This step assumes that voxels which belong to a transition class will lie close to that transition class’s ‘trajectory’ through feature space. The transition line that a voxel is closest to is the selected transition (e.g. NAWM becoming NETTA). This is an important difference versus the traditional approach of separately segmenting and classifying exams at different timepoints. Since only some transitions are allowed (e.g. NAWM is not allowed to become GM), one can correctly assign NAWM as developing a small amount of edema, rather than the typical classification error of assigning it to GM.

In the next step, the actual fractional change is computed. This is separated from the step of deciding the transition, in order to better suppress noise. One noise suppression method applied here is a requirement of spatial coherence. If 1 voxel appears to be

changing from NAWM to NETTA, but none of its neighbors are, the change is rejected as noise. The actual algorithm uses more complex formulas and empirically determined thresholds that we have found to be robust.
At this point, the real change for each voxel is known, and the outputs are produced: colored change maps and numerical values for each transition group.
We applied this change analysis to a series of 99 subjects with brain tumors where there were 3 MRI studies. The first pair showed either no change, or possible change on the initial clinical interpretation. A third exam showed either (1) no change at least 12 months after the second exam (N=50); (2) progression between 3 and 8 months after the second exam (N=30); and (3) progression within 3 months of the second exam (N=19).

Results: We found that certain values for numerical change could separate groups 1 and 3. Specifically, 49 of the 50 'no change' cases were correctly classified while 17 of the 19 'early progressors' were correctly classified. A tantalizing finding is that 21 of the 31 'mid-term' progressors were identified as progressing by the change analysis algorithm, suggesting that the computer algorithm may be able to identify those patients at risk for progressing earlier than human observers.

Conclusions: While further study is required, automated Change Analysis appears useful in detecting and characterizing changes in serial MRI studies such as is used for brain cancer.

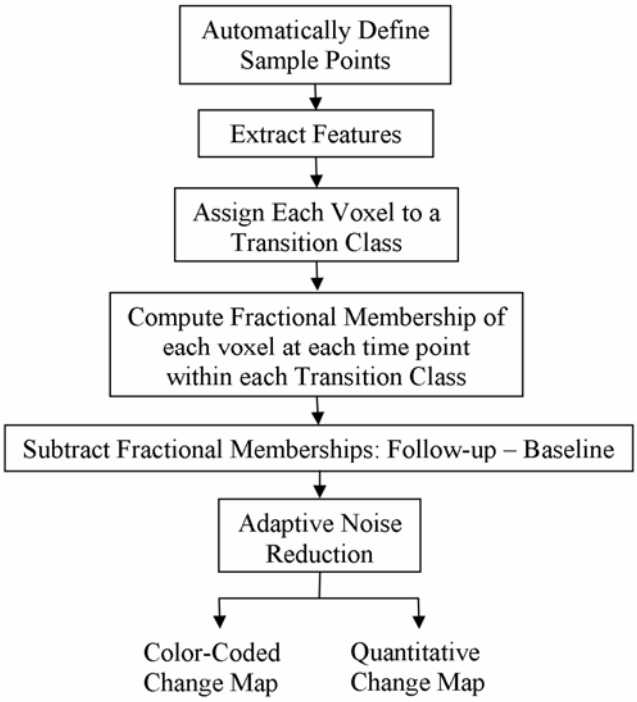

Figure 1.

Reference

1. Sled, J., A. Sijdenbos, and A. Evans, *A nonparametric method for automatic correction of intensity nonuniformity in MRI data.* IEEE Trans Med Imaging, 1998. **17**(1): p. 87-97.